WHAT IS CLAIMED IS:

1. A composition comprising a plurality of positionally distinguishable sequence specific reagents attached to a solid substrate, which reagents are capable of specifically binding to a predetermined subunit sequence of a preselected multi-subunit length having at least three subunits, said reagents representing substantially all possible sequences of said preselected length.

2. A composition of Claim 1, wherein said subunit sequence is a polynucleotide or a polypeptide.

3. A composition of Claim 1, wherein said preselected multi-subunit length is five subunits and said subunit sequence is a polynucleotide sequence.

4. A composition of Claim 1, wherein said specific reagent is an oligonucleotide of at least about five nucleotides.

5. A composition of Claim 1, wherein said specific reagent is a monoclonal antibody.

6. A composition of Claim 1, wherein said specific reagents are all attached to a single solid substrate.

7. A composition of Claim 1, wherein said reagents comprise about 3000 different sequences.

8. A composition of Claim 1, wherein said reagents represents at least about 25% of the possible subsequences of said preselected length.

9. A composition of Claim 1, wherein said reagents are localized in regions of the substrate having a density of at least 25 regions per square centimeter.

10. A composition of Claim 6, wherein said substrate has a surface area of less than about 4 square centimeters.

11. A method of analyzing a sequence of a polynucleotide or a polypeptide, said method comprising the step of:

a) exposing said polynucleotide or polypeptide to a composition of Claim 1.

12. A method of identifying or comparing a target sequence with a reference, said method comprising the step of:

a) exposing said target sequence to a composition of Claim 1;

b) determining the pattern of positions of said reagents which specifically interact with said target sequence; and

c) comparing said pattern with the pattern exhibited by said reference when exposed to said composition.

13. A method for sequencing a segment of a polynucleotide comprising the steps of:

a) combining:

i) a substrate comprising a plurality of chemically synthesized and positionally distinguishable oligonucleotides capable of recognizing defined oligonucleotide sequences; and

ii) a target polynucleotide; thereby forming high fidelity matched duplex structures of complementary subsequences of known sequence; and

b) determining which of said reagents have specifically interacted with subsequences in said target polynucleotide.

14. A method of Claim 13, wherein said segment is substantially the entire length of said polynucleotide.

15. A method for sequencing a polymer, said method comprising the steps of:

a) preparing a plurality of reagents which each specifically bind to a subsequence of preselected length;

b) positionally attaching each of said reagents to one or more solid phase substrates, thereby producing substrates of

positionally definable sequence specific probes;

c) combining said substrates with a target polymer whose sequence is to be determined; and

d) determining which of said reagents have specifically interacted with subsequences in said target polymer.

16. A method of Claim 15, wherein said substrates are beads.

17. A method of Claim 15, wherein said plurality of reagents comprise substantially all possible subsequences of said preselected length found in said target.

18. A method of Claim 15, wherein said solid phase substrates are a single substrate having attached thereto reagents recognizing substantially all possible subsequences of preselected length found in said target.

19. A method of Claim 15, further comprising the step of analyzing a plurality of said recognized subsequences to assemble a sequence of said target polymer.

20. A method of Claim 16, wherein at least some of said plurality of substrates have one subsequence specific reagent attached thereto, and said substrates are coded to indicate the specificity of said reagent.

21. A method of using a fluorescent nucleotide to detect interactions with oligonucleotide probes of known sequence, said method comprising:

a) attaching said nucleotide to a target unknown polynucleotide sequence, and

b) exposing said target polynucleotide sequence to a collection of positionally defined oligonucleotide probes of known sequences to determine the sequences of said probes which interact with said target.

22. A method of Claim 21, further comprising the step of:

a) collating said known sequences to determine the overlaps of said known sequences to determine the sequence of said target sequence.

23. A method of mapping a plurality of sequences relative to one another, said method comprising:

a) preparing a substrate having a plurality of positionally attached sequence specific probes are attached;

b) exposing each of said sequences to said substrate, thereby determining the patterns of interaction between said sequence specific probes and said sequences; and

c) determining the relative locations of said sequence specific probe interactions on said sequences to determine the overlaps and order of said sequences.

24. A method of Claim 23, wherein said sequence specific probes are oligonucleotides.

25. A method of Claim 23, wherein said sequences are nucleic acid sequences.